

## \* **(**

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Tyr Ile Gly Gln His Asp Glu Arg Arg Ala Trp Ile Thr Gly Phe Thr 90

Gly Ser Ala Gly Thr Ala Val Val Thr Met Lys Lys Ala Ala Val Trp 105 100

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Pro Tyr Asn Pro Phe Phe Tyr Ser Tyr Thr Leu Leu Thr Asp Ser Ser 260 265 270

Ile Arg Leu Phe Ala Asn Lys Ser Arg Phe Ser Ser Glu Thr Leu Ser 275 280 285

Tyr Leu Asn Ser Ser Cys Thr Gly Pro Met Cys Val Gln Ile Glu Asp 290 295 300

Tyr Ser Gln Val Arg Asp Ser Ile Gln Ala Tyr Ser Leu Gly Asp Val 305 310 315 320

Arg Ile Trp Ile Gly Thr Ser Tyr Thr Met Tyr Gly Ile Tyr Glu Met 325 330 335

Ile Pro Arg Glu Lys Leu Val Thr Asp Thr Tyr Ser Pro Val Met Met

340 345 350

Thr Lys Ala Val Lys Asn Ser Lys Glu Gln Ala Leu Leu Lys Ala Ser 355 360 365

His Val Arg Asp Ala Val Ala Val Ile Arg Tyr Leu Val Trp Leu Glu 370 375 380

Lys Asn Val Pro Lys Gly Thr Val Asp Glu Phe Ser Gly Ala Glu Ile 385 390 395 400

Val Asp Lys Phe Arg Gly Glu Glu Gln Phe Ser Ser Gly Pro Ser Phe 405 410 415

Glu Thr Ile Ser Ala Ser Gly Leu Asn Ala Ala Leu Ala His Tyr Ser 420 425 430

Pro Thr Lys Glu Leu Asn Arg Lys Leu Ser Ser Asp Glu Met Tyr Leu 435 440 445

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Asn Leu Ser Ala Tyr Ile Ile Pro Gly Thr Asp Ala His Met Asn Glu 65 70 75 80

Tyr Ile Gly Gln His Asp Glu Arg Arg Ala Trp Ile Thr Gly Phe Thr 85 90 95

Gly Ser Ala Gly Thr Ala Val Val Thr Met Lys Lys Ala Ala Val Trp 100 105 110

Thr Asp Ser Arg Tyr Trp Thr Gln Ala Glu Arg Gln Met Asp Cys Asn 115 120 125

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Leu Thr Glu Ile Pro Ala Gly Gly Arg Val Gly Phe Asp Pro Phe Leu 145 150 155 160

Leu Ser Ile Asp Thr Trp Glu Ser Tyr Asp Leu Ala Leu Gln Gly Ser 165 170 175

Asn Arg Gln Leu Val Ser Ile Thr Thr Asn Leu Val Asp Leu Val Trp 180 185 190

Gly Ser Glu Arg Pro Pro Val Pro Asn Gln Pro Ile Tyr Ala Leu Gln 195 200 205

Glu Ala Phe Thr Gly Ser Thr Trp Gln Glu Lys Val Ser Gly Val Arg 210 215 220

Ser Gln Met Gln Lys His Gln Lys Val Pro Thr Ala Val Leu Leu Ser 225 230 235 240

Ala Leu Glu Glu Thr Ala Trp Leu Phe Asn Leu Arg Ala Ser Asp Ile 245 250 255

Pro Tyr Asn Pro Phe Phe Tyr Ser Tyr Thr Leu Leu Thr Asp Ser Ser 260 265 270

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Tyr Leu Asn Ser Ser Cys Thr Gly Pro Met Cys Val Gln Ile Glu Asp 290 295 300 Tyr Ser Gln Val Arg Asp Ser Ile Gln Ala Tyr Ser Leu Gly Asp Val 305 310 315 320

Arg Ile Trp Ile Gly Thr Ser Tyr Thr Met Tyr Gly Ile Tyr Glu Met 325 330 335

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His Val Arg Asp Ala Val Ala Val Ile Arg Tyr Leu Val Trp Leu Glu 370 375 380

Lys Asn Val Pro Lys Gly Thr Val Asp Glu Phe Ser Gly Ala Glu Ile 385 390 395 400

Val Asp Lys Phe Arg Gly Glu Glu Gln Phe Ser Ser Gly Pro Ser Phe 405 410 415

Glu Thr Ile Ser Ala Ser Gly Leu Asn Ala Ala Leu Ala His Tyr Ser 420 425 430

Pro Thr Lys Glu Leu Asn Arg Lys Leu Ser Ser Asp Glu Met Tyr Leu 435 440 445

Leu Asp Ser Gly Gly Gln Tyr Trp Asp Gly Thr Thr Asp Ile Thr Arg 450 460

Thr Val His Trp Gly Thr Pro Ser Ala Phe Gln Lys Glu Ala Tyr Thr 465 470 475 480

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Asp Ala Gly Leu Asn Tyr Gly His Gly Thr Gly His Gly Ile Gly Asn 515 520 525

Phe Leu Cys Val His Glu Trp Pro Val Gly Phe Gln Ser Asn Asn Ile

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Ala Ly	ys Thr	Lys 580	Tyr	Pro	Gly	Glu	Leu 585	Pro	Asp	Leu	Val	Val 590	Ser	Phe	
Val Pr	co Tyr 595	Asp	Arg	Asn	Leu	Ile 600	Asp	Val	Ser	Leu	Leu 605	Ser	Pro	Glu	
His Le	eu Gln 10	Tyr	Leu	Asn	Arg 615	Tyr	Tyr	Gln	Thr	Ile 620	Arg	Glu	Lys	Val	
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310

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Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala

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Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val 115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala 130 135 140

Ser Gly Arg Gln Gln Arg Arg Gln Ala Arg Val Thr Cys Val Leu 145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg 165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu 180 185 190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile 195 200 205

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Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser 70 75 80

Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu 85 90 95

Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe 100 105 110

Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr 115 120 125

Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser 130 135 140

Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu 165 170 175

Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro Met 180 185 190

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Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr 210 215 220

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Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg 50 55 60

Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser 70 75 80

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn 85 90 95

Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro 100 105 110

Ile Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe 115 120 125

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala 130 135 140

Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu 145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser 165 170 175

Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr 180 185 190

Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro 195 200 205 Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp 210 215 220

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Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr 245 250 255

Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr 260 265 270

Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu 275 280 285

Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile 290 295 300

Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe 305 310 315 320

Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met 325 330 335

Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser 340 345 350

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tgc aag ttc cac aac ttc ttc ccc atc gcc gct gtc ttc gcc agt atc Cys Lys Phe His Asn Phe Phe Pro Ile Ala Ala Val Phe Ala Ser Ile 105 110 115 120	570
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Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp  $100\,$ 

Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr 115 120 125

Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp 130 135 140

Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser 165 170 175

Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn 180 185 190

Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln 195 200 205

Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile 210 215 220

Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser 225 230 235 240

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Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile 305 310 315 320

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Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu 370 375 380

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Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu 435 440 445

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Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala 65 70 75 80

Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr 85 90 95

Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp 100 105 110

Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr

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330

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn

345

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Ile	Lys	Val	Thr	Thr 405	Ser	Gln	Asp	Met	Leu 410	Ser	Ile	Met	Glu	Lys 415	Leu	
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Ala 465	Arg	Thr	Leu	Leu	Val 470	Phe	Glu	Val	Gln	Gln 475	Pro	Phe	Leu	Phe	Val 480	
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Val Ile Ser Lys Met Leu Phe Ala Glu Pro Ile Leu Glu Val Ser Ser 50 55 60

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Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp 100 105 110

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Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met 145 150 155 160

Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser 165 170 175

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Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser 225 230 235 240

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Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile 305 310 315 320

Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile 325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn 340 345 350

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Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu

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140

135

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Ile	Trp	Val	Val	Gly 165	Gly	Leu	Leu	Ser	Ile 170	Pro	Thr	Phe	Leu	Leu 175	Arg
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Ile 225	Leu	Ala	Ser	Leu	Arg 230	Thr	Arg	Glu	Glu	Val 235	Ser	Arg	Thr	Arg	Val 240
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Phe	Ile 290	Asp	Leu	Gly	Leu	Gln 295	Leu	Ala	Asn	Phe	Phe 300	Ala	Phe	Thr	Asn
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atc tta gcc cac aaa aga atg agg aca gtg acg aac tat ttt ctg gtg Ile Leu Ala His Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Leu Val 60 65 70	426
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aac ttc acc tat gct gtc cac aac gaa tgg tac tac ggc ctg ttc tac Asn Phe Thr Tyr Ala Val His Asn Glu Trp Tyr Tyr Gly Leu Phe Tyr 90 95 100	522
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Pro	Leu	Gln	Pro 140	Arg	Leu	Ser	Ala	Thr 145	Ala	Thr	Lys	Val	Val 150	Ile	Cys	
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The first first first first tree in the first first of the first f

Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Thr Ser Val Val

Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg 50  $\phantom{0}$  55  $\phantom{0}$  60

Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser 65 70 75 80

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn 85 90 95

Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Xaa Pro 100 105 110

Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe 115 120 125

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala 130 135 140

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Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr 180 185 190

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Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr 245 250 255

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275 280 285

Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile 290 295 300

Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe 305 310 315 320

Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met 325 330 335

Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser 340 345 350

Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu 355 360 365

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<223> wherein N is either a "G" or an "A".

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      wherein Xaa is either "Val" or "Ala".
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      (159)..(159)
<223> wherein Xaa is either "Ala" or "Gly".
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wherein Xaa is either "Val" or "Met".

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VARIANT

(480)..(480)

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Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr 35 40 45

Val Ile Ser Lys Met Leu Phe Xaa Glu Pro Ile Leu Glu Val Ser Ser 50 55 60

Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala 65 70 75 80

Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr 85 90 95

Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp 100 Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr 120 Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp 135 Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Xaa Met 150 155 Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser 165 170 Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn 185 Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln 200 Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile 215 Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser 230 235 Arg Thr Leu Tyr Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp 245 250 Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn 260 265 Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val 280 Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp 295 Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile 310 315 Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile 325 Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu 355 360 Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg 390 395

Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu 405 410 Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val 450 455 Ala Arg Thr Leu Leu Val Phe Glu Val Gln Pro Phe Leu Phe Xaa 465 470 475 Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr 485 490

Asp Pro Arg Ala 500

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<222> (592)..(592)

<223> wherein N is either an "A" or a "G".

<220> <221> misc\_feature <222> (469)..(469)

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<223> wherein N is either a "G" or a "C".

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60

120

180

240

300

360

420

480

133

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<223> wherein Xaa is either "Lys" or "Glu".

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Gln Cys Gly Gly Ile Leu Val His Arg Gln Trp Val Leu Thr Ala Ala 50 55 60

His Cys Ile Ser Asp Asn Tyr Gln Leu Trp Leu Gly Arg His Asn Leu 65 70 75 80

Phe Asp Asp Glu Asn Thr Ala Gln Phe Val His Val Ser Glu Ser Phe 85 90 95

Pro His Pro Gly Phe Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln
100 105 110

Ala Asp Glu Asp Tyr Ser His Asp Leu Met Leu Leu Arg Leu Thr Glu 115 120 125

Pro Ala Asp Thr Ile Thr Asp Ala Val Lys Val Val Glu Leu Pro Thr

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Le	ı Lys	: Ile	Leu 180	Pro	Asn	Asp	Glu	Cys 185	Xaa	Lys	Ala	His	Val 190	Gln	Lys	
Va	l Thi	195		Met	Leu	Cys	Val 200	Gly	His	Leu	Glu	Gly 205	Gly	Lys	Asp	
Th	r Cys 210	val	Gly	Asp	Ser	Gly 215	Gly	Pro	Leu	Met	Cys 220	Asp	Gly	Val	Leu	
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<sup>&</sup>lt;213> Homo sapiens

<sup>&</sup>lt;400> 558

		35					40					45			
Phe	Phe 50	Gly	Leu	Leu	Gly	Asn 55	Leu	Phe	Val	Leu	Leu 60	Val	Phe	Leu	Leu
Pro 65	Arg	Arg	Gln	Leu	Asn 70	Val	Ala	Glu	Ile	Tyr 75	Leu	Ala	Asn	Leu	Ala 80
Ala	Ser	Asp	Leu	Val 85	Phe	Val	Leu	Gly	Leu 90	Pro	Phe	Trp	Ala	Glu 95	Asn
Ile	Trp	Asn	Gln 100	Phe	Asn	Trp	Pro	Phe 105	Gly	Ala	Leu	Leu	Cys 110	Arg	Val
Ile	Asn	Gly 115	Val	Ile	Lys	Ala	Asn 120	Leu	Phe	Ile	Ser	Ile 125	Phe	Leu	Val
Val	Ala 130	Ile	Ser	Gln	Asp	Arg 135	Tyr	Arg	Val	Leu	Val 140	His	Pro	Met	Ala
Ser 145	Gly	Arg	Gln	Gln	Arg 150	Arg	Arg	Gln	Ala	Arg 155	Val	Thr	Cys	Val	Leu 160
Ile	Trp	Val	Val	Gly 165	Gly	Leu	Leu	Ser	Ile 170	Pro	Thr	Phe	Leu	Leu 175	Arg
Ser	Ile	Gln	Ala 180	Val	Pro	Asp	Leu	Asn 185	Ile	Thr	Ala	Cys	Ile 190	Leu	Leu
Leu	Pro	His 195	Glu	Ala	Trp	His	Phe 200	Ala	Arg	Ile	Val	Glu 205	Leu	Asn	Ile
Leu	Gly 210	Phe	Leu	Leu	Pro	Leu 215	Ala	Ala	Ile	Val	Phe 220	Phe	Asn	Tyr	His
Ile 225	Leu	Ala	Ser	Leu	Arg 230	Thr	Arg	Glu	Glu	Val 235	Ser	Arg	Thr	Arg	Val 240
Arg	Gly	Pro	Lys	Asp 245	Ser	Lys	Thr	Thr	Ala 250	Leu	Ile	Leu	Thr	Leu 255	Val
Val	Ala	Phe	Leu 260	Val	Cys	Trp	Ala	Pro 265		His	Phe	Phe	Ala 270		Leu
Glu	Phe	Leu 275	Phe	Gln	Val	Gln	Ala 280	Val	Arg	Gly	Cys	Phe 285	Trp	Glu	Asp
Phe	Ile 290	Asp	Leu	Gly	Leu	Gln 295	Leu	Ala	Asn	Phe	Phe 300	Ala	Phe	Thr	Asr
Ser 305	Ser	Leu	Asn	Pro	Val 310	Ile	Tyr	Val	Phe	Val 315	Gly	Arg	Leu	Phe	Arg 320
Thr	Lys	Val	Trp	Glu 325	Leu	Tyr	Lys	Gln	Cys 330	Thr	Pro	Lys	Ser	Leu 335	Ala

Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg

340 345 350

Asn

<210> 559
<211> 1082
<212> DNA
<213> Homo sapiens
<220>
<221> misc\_feature
<222> (577)..(577)
<223> wherein N is either a "C" or a "G".

<400> 559 ctgtgcatgg catcatcctg gccccctcta gagctccaat cctccaacca gagccagctc 60 120 ttccctcaaa atgctacggc ctgtgacaat gctccagaag cctgggacct gctgcacaga 180 gtgctgccga catttatcat ctccatctgt ttcttcggcc tcctagggaa cctttttgtc 240 ctgttggtct tcctcctgcc ccggcggcaa ctgaacgtgg cagaaatcta cctggccaac 300 ctggcagcct ctgatctggt gtttgtcttg ggcttgccct tctgggcaga gaatatctgg aaccagttta actggccttt cggagccctc ctctgccgtg tcatcaacgg ggtcatcaag 360 420 gccaatttgt tcatcagcat cttcctggtg gtggccatca gccaggaccg ctaccgcgtg ctggtgcacc ctatggccag cggaaggcag cagcggcgga ggcaggcccg ggtcacctgc 480 gtgctcatct gggttgtggg gggcctcttg agcatcccca cattcctgct gcgatccatc 540 600 caageegtee cagatetgaa cateacegee tgeategtge teeteeeca tgaggeetgg 660 cactttgcaa ggattgtgga gttaaatatt ctgggtttcc tcctaccact ggctgcgatc 720 gtcttcttca actaccacat cctggcctcc ctgcgaacgc gggaggaggt cagcaggaca agagtgcggg ggccgaagga tagcaagacc acagcgctga tcctcacgct cgtggttgcc 780 ttcctggtct gctgggcccc ttaccacttc tttgccttcc tggaattctt attccaggtg 840 900 caagcagtcc gaggctgctt ttgggaggac ttcattgacc tgggcctgca attggccaac 960 ttctttgcct tcactaacag ctccctgaat ccagtaattt atgtctttgt gggccggctc ttcaggacca aggtctggga actttataaa caatgcaccc ctaaaagtct tgctccaata 1020 tcttcatccc ataggaaaga aatcttccaa cttttctggc ggaattaaaa cagcattgaa 1080 1082 CC

<210> 560

<211> 353 <212> PRT <213> Homo sapiens <220> <221> VARIANT <222> (191)..(191) <223> wherein Xaa is either "Leu" or "Val". <400> 560 Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn Gln Ser Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys 40

Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu 50 55 60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala 65 70 75 80

Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn 85 90 95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val 100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val 115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala 130 135 140

Ser Gly Arg Gln Gln Arg Arg Gln Ala Arg Val Thr Cys Val Leu 145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg 165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Val Leu 180 185 190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile
195 200 205

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His 210 215 220

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val 225 230 235 240

<221>

<222>

<400> 561

misc\_feature

(705)..(705)

wherein N is either a "G" or an "A".

Arg	Gly	Pro	Lys	Asp 245	Ser	Lys	Thr	Thr	Ala 250	Leu	Ile	Leu	Thr	Leu 255	Val
Val	Ala	Phe	Leu 260	Val	Cys	Trp	Ala	Pro 265	Tyr	His	Phe	Phe	Ala 270	Phe	Leu
Glu	Phe	Leu 275	Phe	Gln	Val	Gln	Ala 280	Val	Arg	Gly	Cys	Phe 285	Trp	Glu	Asp
Phe	Ile 290	Asp	Leu	Gly	Leu	Gln 295	Leu	Ala	Asn	Phe	Phe 300	Ala	Phe	Thr	Asn
Ser 305	Ser	Leu	Asn	Pro	Val 310	Ile	Tyr	Val	Phe	Val 315	Gly	Arg	Leu	Phe	Arg 320
Thr	Lys	Val	Trp	Glu 325	Leu	Tyr	Lys	Gln	Cys 330	Thr	Pro	Lys	Ser	Leu 335	Ala
Pro	Ile	Ser	Ser 340	Ser	His	Arg	Lys	Glu 345	Ile	Phe	Gln	Leu	Phe 350	Trp	Arg
Asn															
<210 <210 <210 <210	1> 2> :	561 1082 DNA Homo	gan	i ens											
<22		1101110	Бар	10115											

60 ctgtgcatgg catcatcctg gcccctcta gagctccaat cctccaacca gagccagctc ttccctcaaa atgctacggc ctgtgacaat gctccagaag cctgggacct gctgcacaga 120 gtgctgccga catttatcat ctccatctgt ttcttcggcc tcctagggaa cctttttgtc 180 ctgttggtct tcctcctgcc ccggcggcaa ctgaacgtgg cagaaatcta cctggccaac 240 ctggcagcct ctgatctggt gtttgtcttg ggcttgccct tctgggcaga gaatatctgg 300 aaccagttta actggccttt cggagccctc ctctgccgtg tcatcaacgg ggtcatcaag 360 420 gccaatttgt tcatcagcat cttcctggtg gtggccatca gccaggaccg ctaccgcgtg ctggtgcacc ctatggccag cggaaggcag cagcggcgga ggcaggcccg ggtcacctgc 480 gtgctcatct gggttgtggg gggcctcttg agcatcccca cattcctgct gcgatccatc 540 600 caagccgtcc cagatctgaa catcaccgcc tgcatcctgc tcctccccca tgaggcctgg

cactttgcaa ggattgtgga gttaaatatt ctgggtttcc tcctaccact ggctgcgatc

gtcttcttca	actaccacat	cctggcctcc	ctgcgaacgc	gggaggaggt	cagcaggaca	720
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ttctttgcct	tcactaacag	ctccctgaat	ccagtaattt	atgtctttgt	gggccggctc	960
ttcaggacca	aggtctggga	actttataaa	caatgcaccc	ctaaaagtct	tgctccaata	1020
tcttcatccc	ataggaaaga	aatcttccaa	cttttctggc	ggaattaaaa	cagcattgaa	1080
CC						1082

<210> 562

<211> 353 <212> PRT

<213> Homo sapiens

<400> 562

Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn Gln Ser 1 5 10 15

Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala 20 25 30

Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys 35 40 45

Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu 50 55 60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala 65 70 75 80

Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn 85 90 95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val 100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val 115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala 130 135 140

Ser Gly Arg Gln Gln Arg Arg Gln Ala Arg Val Thr Cys Val Leu 145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg 165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu 180 185 190									
Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile 195 200 205									
Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His 210 215 220									
Ile Leu Ala Ser Leu Arg Thr Arg Lys Glu Val Ser Arg Thr Arg Val 225 230 235 240									
Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val 245 250 255									
Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu 260 265 270									
Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp 275 • 280 285									
Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn 290 295 300									
Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg 305 310 315 320									
Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala 325 330 335									
Pro Ile Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg 340 345 350									
Asn									
<210> 563 <211> 3733 <212> DNA <213> Homo sapiens									
<220> <221> misc_feature <222> (40)(40) <223> wherein N is either a "C" or a "T".									
<400> 563 atgttctctc cctggaagat atcaatgttt ctgtctgttt gtgaggactc cgtgcccacc									
acggcctctt tcagcgccga catgctcaat gtcaccttgc aagggcccac tcttaacggg									
acctttgccc agagcaaatg cccccaagtg gagtggctgg gctggctcaa caccatccag									

cccccttcc tctgggtgct gttcgtgctg gccaccctag agaacatctt tgtcctcagc

300 gtcttctgcc tgcacaagag cagctgcacg gtggcagaga tctacctggg gaacctggcc gcagcagacc tgatcctggc ctgcgggctg cccttctggg ccatcaccat ctccaacaac 360 ttcgactggc tctttgggga gacgctctgc cgcgtggtga atgccattat ctccatgaac 420 480 ctgtacagca gcatctgttt cctgatgctg gtgagcatcg accgctacct ggccctggtg 540 aaaaccatgt ccatgggccg gatgcgcggc gtgcgctggg ccaagctcta cagcttggtg atctgggggt gtacgctgct cctgagctca cccatgctgg tgttccggac catgaaggag 600 660 tacagcgatg agggccacaa cgtcaccgct tgtgtcatca gctacccatc cctcatctgg 720 gaagtgttca ccaacatgct cctgaatgtc gtgggcttcc tgctgcccct gagtgtcatc accttctgca cgatgcagat catgcaggtg ctgcggaaca acgagatgca gaagttcaag 780 840 gagatccaga cggagaggag ggccacggtg ctagtcctgg ttgtgctgct gctattcatc 900 atctgctggc tgcccttcca gatcagcacc ttcctggata cgctgcatcg cctcggcatc 960 ctctccagct gccaggacga gcgcatcatc gatgtaatca cacagatcgc ctccttcatg 1020 gcctacagca acagctgcct caacccactg gtgtacgtga tcgtgggcaa gcgcttccga 1080 aagaagtett gggaggtgta ceagggagtg tgeeagaaag ggggetgeag gteagaacee attcagatgg agaactccat gggcacactg cggacctcca tctccgtgga acgccagatt 1140 1200 cacaaactgc aggactgggc agggagcaga cagtgagcaa acgccagcag ggctgctgtg 1260 aatttgtgta aggattgagg gacagttgct tttcagcatg ggcccaggaa tgccaaggag 1320 acatctatgc acgaccttgg gaaatgagtt gatgtctccg gtaaaacacc ggagactaat 1380 tcctgccctg cccaattttg cagggagcat ggctgtgagg atggggtgaa ctcacgcaca 1440 gccaaggact ccaaaatcac aacagcatta ctgttcttat ttgctgccac acctgagcca gcctgctcct tcccaggagt ggaggaggcc tggggggagg gagaggagtg actgagcttc 1500 1560 cctcccgtgt gttctccgtc cctgccccag caagacaact tagatctcca ggagaactgc catccagctt tggtgcaatg gctgagtgca caagtgagtt gttgccctgg gtttctttaa 1620 1680 tctattcagc tagaactttg aaggacaatt tcttgcatta ataaaggtta agccctgagg 1740 ggtccctgat aacaacctgg agaccaggat tttatggctc ccctcactga tggacaagga 1800 ggtctgtgcc aaagaagaat ccaataagca catattgagc acttgctgta tatgcagtat tgagcactgt aggcaagacc caagaaagag aaggagccat ctccatcttg aaggaactca 1860 aagactcaag tgggaacgac tgggcactgc caccaccaga aagctgttcg acgagacggt 1920 cgagcagggt gctgtgggtg atatggacag cagaaggggg agaccaaggt tccagctcaa 1980

ccaataacta	ı ttgcacaacc	acctgtccct	gcctcagttc	ccttttatgt	aacatgaagt	2040
cgttgtgagg	gttaaaggca	gtaacaggta	taaagtactt	agaaaagcaa	agggtgctac	2100
gtacatgtga	ggcatcatta	cgcagacgta	actgggatat	gtttactata	aggaaaagac	2160
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aaagtctgat	ttgtgatgag	gcagaggaag	atatttctaa	tcggtcttgc	ccagaggatc	2400
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agggctggaa	tctggagagc	tagaacctgg	agggctagaa	cctggagggc	tagaacctag	2880
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agaagggcta	gaacctggag	agccagaacc	tggagggcta	gaacctggaa	gggctagaac	3060
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gagcccataa	atcctgacca	atccaactct	gaattttaaa	gcaaaagcgt	gaaaaaaaag	3240
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agaatgaagt	caaactgtgc	cacacatggt	gaatgaaaaa	aaaaaaaag	aggctgtgtt	3420
ttgtcacaca	gggcagtcat	tcagcaccag	agcacgtgat	ggtctgagac	tctcttagga	3480
gcagagctct	gccgcaatgg	ccatgtgggg	atccacacct	ggtctgaggg	gcaactgagt	3540
ctgcgggaga	agagcggccc	tatgcatggt	gtagatgccc	tgataaagaa	catctgtcct	3600
gtgaaagact	caatgagctg	ttatgttgta	aacaggaagc	atttcacatc	caaacgagaa	3660

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aaaaaaaaa	aaa					3733

<210>	564	
<211>	391	
<212>	PRT	
<213>	Homo	sapi

ens

<220> <221> VARIANT <222> (14)..(14)

wherein Xaa is either "Arg" or "Cys".

<400> 564

Met Phe Ser Pro Trp Lys Ile Ser Met Phe Leu Ser Val Cys Glu Asp 10

Ser Val Pro Thr Thr Ala Ser Phe Ser Ala Asp Met Leu Asn Val Thr 25

Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro 40

Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu 55

Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser

Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu 90

Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe 105

Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr 120

Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser 135

Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val 150 155

Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu 165

Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Ser Ser Pro Met 185

Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val 195 200

Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr 210 215 220										
Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile 225 230 235 240										
Thr Phe Cys Thr Met Gln Ile Met Gln Val Leu Arg Asn Asn Glu Met 245 250 255										
Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val 260 265 270										
Leu Val Val Leu Leu Phe Ile Ile Cys Trp Leu Pro Phe Gln Ile 275 280 285										
Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys 290 295 300										
Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met 305 310 315 320										
Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly 325 330 335										
Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln 340 345 350										
Lys Gly Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly 355 360 365										
Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln 370 380										
Asp Trp Ala Gly Ser Arg Gln 385 390										
<210> 565 <211> 3733 <212> DNA <213> Homo sapiens										
<220> <221> misc_feature <222> (933)(933) <223> wherein N is either a "T" or a "C".										
<400> 565 atgttctctc cctggaagat atcaatgttt ctgtctgttc gtgaggactc cgtgcccacc										
acggcctctt tcagcgccga catgctcaat gtcaccttgc aagggcccac tcttaacggg										

acctttgccc agagcaaatg cccccaagtg gagtggctgg gctggctcaa caccatccag

cccccttcc tctgggtgct gttcgtgctg gccaccctag agaacatctt tgtcctcagc

gtcttctgcc tgcacaagag cagctgcacg gtggcagaga tctacctggg gaacctggcc

60

120

180

240

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ttcgactggc	tctttgggga	gacgctctgc	cgcgtggtga	atgccattat	ctccatgaac	420
ctgtacagca	gcatctgttt	cctgatgctg	gtgagcatcg	accgctacct	ggccctggtg	480
aaaaccatgt	ccatgggccg	gatgcgcggc	gtgcgctggg	ccaagctcta	cagcttggtg	540
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ctctccagct	gccaggacga	gcgcatcatc	gacgtaatca	cacagatcgc	ctccttcatg	960
gcctacagca	acagctgcct	caacccactg	gtgtacgtga	tcgtgggcaa	gcgcttccga	1020
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Trp	Ala	11e 115	Thr	Ile	Ser	Asn	Asn 120	Phe	Asp	Trp	Leu	Phe 125	Gly	Glu	Thr
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Lys	Thr	Met	Ser	Met 165	Gly	Arg	Met	Arg	Gly 170	Val	Arg	Trp	Ala	Lys 175	Leu
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Leu	Val	Phe 195	Arg	Thr	Met	Lys	Glu 200	Tyr	Ser	Asp	Glu	Gly 205	His	Asn	Val
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Asn 225	Met	Leu	Leu	Asn	Val 230	Val	Gly	Phe	Leu	Leu 235	Pro	Leu	Ser	Val	Ile 240
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Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met 305 310 315 320										
Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly 325 330 335										
Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln 340 345 350										
Lys Gly Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly 355 360 365										
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Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu 50 55 60

Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser 65 70 75 80

Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu 85 90 95

Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe 100 105 110

Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr
115 120 125

Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser 130 135 140

Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val 145 150 155 160

Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu 165 170 175

Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro Met 180 185 190

Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val

Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr 210 215 220

Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile 225 230 235 240

Thr Phe Cys Thr Met Gln Ile Met Gln Val Leu Arg Asn Asn Glu Met 245 250 255

Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val 260 265 270	
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Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys 290 295 300	
Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met 305 310 315 320	
Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly 325 330 335	
Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln 340 345 350	
Lys Glu Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly 355 360 365	
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Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn 50 55 60

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<sup>&</sup>lt;211> 805

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Homo sapiens

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Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe 390 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys 410 His Leu Lys Ser Ile Gly Leu Leu Ser Pro Asp Phe Gln Glu Asp Asn 425 Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly 440 Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe 455 Lys Gly Glu Ile Pro Lys Asp Gln Trp Met Lys Lys Trp Trp Glu Met 470 Lys Arg Glu Ile Val Gly Val Val Glu Pro Val Pro His Asp Glu Thr 485 490 Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe 505 Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln Phe Gln Phe Gln Glu Ala 520 Leu Cys Gln Ala Ala Lys His Glu Gly Pro Leu His Lys Cys Asp Ile 535 Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Phe Asn Met Leu Arg Leu 550 555 Gly Lys Ser Glu Pro Trp Thr Leu Ala Leu Glu Asn Val Val Gly Ala 570 Lys Asn Met Asn Val Arg Pro Leu Leu Asn Tyr Phe Glu Pro Leu Phe 585 Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser Phe Val Gly Trp Ser Thr 600 Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu 615 Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu Trp Asn Asp Asn Glu Met 630 635 Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Gln Tyr Phe Leu 645 Lys Val Lys Asn Gln Met Ile Leu Phe Gly Glu Glu Asp Val Arg Val 665 Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn Phe Phe Val Thr Ala Pro 680

Lys	Asn 690	Val	Ser	Asp	Ile	Ile 695	Pro	Arg	Thr	Glu	Val 700	Glu	Lys	Ala	Ile		
Arg 705	Met	Ser	Arg	Ser	Arg 710	Ile	Asn	Asp	Ala	Phe 715	Arg	Leu	Asn	Asp	Asn 720		
Ser	Leu	Glu	Phe	Leu 725	Gly	Ile	Gln	Pro	Thr 730	Leu	Gly	Pro	Pro	Asn 735	Gln		
Pro	Pro	Val	Ser 740	Ile	Trp	Leu	Ile	Val 745	Phe	Gly	Val	Val	Met 750	Gly	Val		
Ile	val	Val 755	Gly	Ile	Val	Ile	Leu 760		Phe	Thr	Gly	Ile 765	Arg	Asp	Arg		
Lys	Lys 770		Asn	Lys	Ala	Arg 775		Gly	Glu	Asn	Pro 780	Tyr	Ala	Ser	Ile		
Asr 785	o Ile	Ser	Lys	Gly	Glu 790	Asn	Asn	Pro	Gly	Phe 795	Gln	Asn	Thr	Asp	Asp 800		
Val	l Gln	Thr	Ser	Phe 805													
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cg	cttct	act	acct	gato	gc t	tcgg	gagac	cc cc	gggg	gaaga	a aca	tctt	ttt	ctcc	ccgctg	2	40
																2	^ ^

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tggaacaact	tgttgcggaa	gaggaatttt	tacaagaagc	tagagttgca	tcttcccaag	960
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gtcgtcgacc	ccacgaaacc	atag				1284

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Homo sapiens

<400> 572

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Leu Ser His Gly Gln Leu His Val Glu His Asp Gly Glu Ser Cys Ser 20

Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser

Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr 50

Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu

Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His

Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu

Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu 115

Asn Leu Pro Gly His Gly Leu Glu Thr Arg Val Gly Ser Ala Leu Phe 135

Leu Ser His Asn Leu Lys Phe Leu Ala Lys Phe Leu Asn Asp Thr Met 145 150

Ala Val Tyr Glu Ala Lys Leu Phe His Thr Asn Phe Tyr Asp Thr Val 165 170

Gly Thr Ile Gln Leu Ile Asn Asp His Val Lys Lys Glu Thr Arg Gly 180 185 190

Lys Ile Val Asp Leu Val Ser Glu Leu Lys Lys Asp Val Leu Met Val 195 200 205

Leu Val Asn Tyr Ile Tyr Phe Lys Ala Leu Trp Glu Lys Pro Phe Ile 210 215 220

Ser Ser Arg Thr Thr Pro Lys Asp Phe Tyr Val Asp Glu Asn Thr Thr 225 230 235 240

Val Arg Val Pro Met Met Leu Gln Asp Gln Glu His His Trp Tyr Leu 245 250 255

His Asp Arg Tyr Leu Pro Cys Ser Val Leu Arg Met Asp Tyr Lys Gly 260 265 270

Asp Ala Thr Val Phe Phe Ile Leu Pro Asn Gln Gly Lys Met Arg Glu 275 280 285

Ile Glu Glu Val Leu Thr Pro Glu Met Leu Met Arg Trp Asn Asn Leu 290 295 300

Leu Arg Lys Arg Asn Phe Tyr Lys Lys Leu Glu Leu His Leu Pro Lys 305 310 315

Phe Ser Ile Ser Gly Ser Tyr Val Leu Asp Gln Ile Leu Pro Arg Leu 325 330 335

Gly Phe Thr Asp Leu Phe Ser Lys Trp Ala Asp Leu Ser Gly Ile Thr 340 345 350

Lys Gln Gln Lys Leu Glu Ala Ser Lys Ser Phe His Lys Ala Thr Leu 355 360 365

Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Ala Thr Thr Phe Ala 370 380 .

Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn 385 390 395 400

Arg Pro Phe Leu Val Val Ile Phe Ser Thr Ser Thr Gln Ser Val Leu 405 410 415

Phe Leu Gly Lys Val Val Asp Pro Thr Lys Pro 420 425

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<211> 1284

<212> DNA

<213> Homo sapiens

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cgcttctact	acctgatcgc	ttcggagacc	ccggggaaga	acatctttt	ctccccgctg	240
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<sup>&</sup>lt;210> 574

Met His Leu Ile Asp Tyr Leu Leu Leu Leu Val Gly Leu Leu Ala

<sup>&</sup>lt;211> 427

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Homo sapiens

<sup>&</sup>lt;400> 574

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Asn	Ser	Ser 35	His	Gln	Gln	Ile	Leu 40	Glu	Thr	Gly	Glu	Gly 45	Ser	Pro	Ser
Leu	Lys 50	Ile	e Ala	Pro	Ala	Asn 55	Ala	Asp	Phe	Ala	Phe 60	Arg	Phe	Tyr	Tyr
Leu 65	Ile	Ala	Ser	Glu	Thr 70	Pro	Gly	Lys	Asn	Ile 75	Phe	Phe	Ser	Pro	Leu 80
Ser	Ile	Ser	Ala	Ala 85	Tyr	Ala	Met	Leu	Ser 90	Leu	Gly	Ala	Суѕ	Ser 95	His
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Ser	Glu	Ser 115	Asp	Val	His	Arg	Gly 120	Phe	Gln	His	Leu	Leu 125	His	Thr	Leu
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Ser 225	Ser	Arg	Thr	Thr	Pro 230	Lys	Asp	Phe	Tyr	Val 235	Asp	Glu	Asn	Thr	Thr 240
Val	Arg	Val	Pro	Met 245	Met	Leu	Gln	Asp	Gln 250	Glu	His	His	Trp	Tyr 255	Leu
His	Asp	Arg	Туг 260	Leu	Pro	Cys	Ser	Val 265	Leu	Arg	Met	Asp	Tyr 270	Lys	Gly
Asp	Ala	Thr 275	Val	Phe	Phe	Ile	Leu 280	Pro	Asn	Gln	Gly	Lys 285	Met	Arg	Glu
Ile	Glu 290	Glu	Val	Leu	Thr	Pro 295	Glu	Met	Leu	Met	Arg 300	Trp	Asn	Asn	Leu
Leu	Arg	Lys	Arg	Asn	Phe	Tyr	Lys	Lys	Leu	Glu	Leu	His	Leu	Pro	Lys

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Asp Va		Glu	Ala	Gly	Thr 375	Glu	Ala	Ala	Ala	Ala 380	Thr	Thr	Phe	Ala	
Ile Ly 385	s Phe	Phe	Ser	Ala 390	Gln	Thr	Asn	Arg	His 395	Ile	Leu	Arg	Phe	Asn 400	
Arg Pr	o Phe	Leu	Val 405	Val	Ile	Phe	Ser	Thr 410	Ser	Thr	Gln	Ser	Val 415	Leu	
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Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser 35 40 45

Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr 50 55 60

Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu 65 70 75 80

Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His 85 90 95

Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu 100 105 110

Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu 115 120 125

Asn Leu Pro Gly His Gly Leu Glu Thr Arg Val Gly Ser Ala Leu Phe 130 140

1284

DNA

<212>

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       wherein N is either a "C" or a "G".
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       (412)..(412)
       wherein N is either a "C" or a "T".
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       wherein N is either a "T" or a "C".
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                                                                      120
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<210> 578

<211> 427

<212> PRT

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<221> VARIANT

<222> (138)..(138)

<223> wherein Xaa is either "Arg" or a "Cys".

<400> 578

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Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser 35 40 45

Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr 50 55 60

Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu 70 75 80

Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His 85 90 95

Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu 100 105 110

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Trp	Asp	Leu 35	Leu	His	Arg	Val	Leu 40	Pro	Thr	Phe	Ile	Ile 45	Ser	Ile	Cys	
Phe	Phe 50	Gly	Leu	Leu	Gly	Asn 55	Leu	Phe	Val	Leu	Leu 60	Val	Phe	Leu	Leu	
Pro 65	Arg	Arg	Gln	Leu	Asn 70	Val	Ala	Glu	Ile	Tyr 75	Leu	Ala	Asn	Leu	Ala 80	
Ala	Ser	Asp	Leu	Val 85	Phe	Val	Leu	Gly	Leu 90	Pro	Phe	Trp	Ala	Glu 95	Asn	
Ile	Trp	Asn	Gln 100	Phe	Asn	Trp	Pro	Phe 105	Gly	Ala	Leu	Leu	Cys 110	Arg	Val	
Ile	Asn	Gly 115	Val	Ile	Lys	Ala	Asn 120	Leu	Phe	Ile	Ser	Ile 125	Phe	Leu	Val	
Val	Ala 130	Ile	Ser	Gln	Asp	Arg 135	Tyr	Arg	Val	Leu	Val 140	His	Pro	Met	Ala	
Ser 145	Gly	Arg	Gln	Gln	Arg 150	Arg	Arg	Gln	Ala	Arg 155	Val	Thr	Cys	Val	Leu 160	
Ile	Trp	Val	Val	Gly	Gly	Leu	Leu	Ser	Ile	Pro	Thr	Phe	Leu	Leu	Arg	

165 170 175 Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu 185 Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val 250 Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp 280 Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn 300 Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala 330 Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg Asn <210> 836 <211> 352 <212> PRT <213> Oryctolagus cuniculus <400> 836 Met Ala Ser Gln Gly Pro Leu Glu Leu Gln Pro Ser Asn Gln Ser Gln 10 Leu Ala Pro Pro Asn Ala Thr Ser Cys Ser Gly Ala Pro Asp Ala Trp

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60

<212> PRT

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<400> 837

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Asp Leu Leu Tyr Arg Val Leu Pro Gly Phe Val Ile Thr Ile Cys Phe 35 40 45

Phe Gly Leu Leu Gly Asn Leu Leu Val Leu Ser Phe Phe Leu Leu Pro 50 55 60

Trp Arg Gln Trp Trp Gln Gln Arg Gln Arg Gln Gln Arg Leu Thr 65 70 75 80

Ile Ala Glu Ile Tyr Leu Ala Asn Leu Ala Ala Ser Asp Leu Val Phe 85 90 95

Val Leu Gly Leu Pro Phe Trp Ala Glu Asn Ile Gly Asn Arg Phe Asn 100 105 110

Trp Pro Phe Gly Thr Asp Leu Cys Arg Val Val Ser Gly Val Ile Lys
115 120 125

Ala Asn Leu Phe Val Ser Ile Phe Leu Val Val Ala Ile Ser Gln Asp 130 135 140

Arg Tyr Arg Leu Leu Val Tyr Pro Met Thr Ser Trp Gly Tyr Arg Arg 145 150 155 160

Arg Arg Gln Ala Gln Ala Thr Cys Leu Leu Ile Trp Val Ala Gly Gly 165 170 175

Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg Ser Val Lys Val Val Pro 180 185 190

Asp Leu Asn Val Ser Ala Cys Ile Leu Leu Phe Pro His Glu Ala Trp 195 200 205

His Phe Ala Arg Met Val Glu Leu Asn Val Leu Gly Phe Leu Leu Pro 210 215 220

Val Thr Ala Ile Ile Phe Phe Asn Tyr His Ile Leu Ala Ser Leu Arg 225 230 235 240

Gly Gln Lys Glu Ala Ser Arg Thr Arg Cys Gly Gly Pro Lys Gly Ser 245 250 255

Lys Thr Thr Gly Leu Ile Leu Thr Leu Val Ala Ser Phe Leu Val Cys 260 265 270

Trp Cys Pro Tyr His Phe Phe Ala Phe Leu Asp Phe Leu Val Gln Val 275 280 285 Arg Val Ile Gln Asp Cys Ser Trp Lys Glu Ile Thr Asp Leu Gly Leu 290 295 300

Gln Leu Ala Asn Phe Phe Ala Phe Val Asn Ser Cys Leu Asn Pro Leu 305 310 315 320

Ile Tyr Val Phe Ala Gly Arg Leu Leu Lys Thr Arg Val Leu Gly Thr 325 330 335

Leu

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<213> Mus musculus

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Met Pro Thr Ala Ala Ser Phe Gly Ile Glu Met Phe Asn Val Thr Thr 20 25 30

Gln Val Leu Gly Ser Ala Leu Asn Gly Thr Leu Ser Lys Asp Asn Cys 35 40 45

Pro Asp Thr Glu Trp Trp Ser Trp Leu Asn Ala Ile Gln Ala Pro Phe 50 55 60

Leu Trp Val Leu Phe Leu Leu Ala Ala Leu Glu Asn Leu Phe Val Leu 65 70 75 80

Ser Val Phe Phe Leu His Lys Asn Ser Cys Thr Val Ala Glu Ile Tyr 85 90 95

Leu Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro 100 105 110

Phe Trp Ala Ile Thr Ile Ala Asn Asn Phe Asp Trp Val Phe Gly Glu 115 120 125

Val Leu Cys Arg Val Val Asn Thr Met Ile Tyr Met Asn Leu Tyr Ser 130 135 140

Ser Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu 145 150 155 160

Val Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys 165 170 175

Leu Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro 180 185 190

Met Leu Val Phe Arg Thr Met Arg Glu Tyr Ser Glu Glu Gly His Asn

		195					200					205	i		
Val	Thr 210	Ala	Cys	Val	Ile	Val 215		Pro	Ser	Arg	Ser 220	Trp	Glu	. Val	Phe
Thr 225	Asn	Val	Leu	Leu	Asn 230	Leu	Val	Gly	Phe	Leu 235	Leu	Pro	Leu	Ser	Val 240
Ile	Thr	Phe	Cys	Thr 245	Val	Arg	Ile	Leu	Gln 250	Val	Leu	Arg	Asn	Asn 255	
Met	Lys	Lys	Phe 260	Lys	Glu	Val	Gln	Thr 265	Glu	Arg	Lys	Ala	Thr 270	Val	Leu
Val	Leu	Ala 275	Val	Leu	Gly	Leu	Phe 280	Val	Leu	Cys	Trp	Val 285	Pro	Phe	Gln
Ile	Ser 290	Thr	Phe	Leu	Asp	Thr 295	Leu	Leu	Arg	Leu	Gly 300	Val	Leu	Ser	Gly
Cys 305	Trp	Asp	Glu	His	Ala 310	Val	Asp	Val	Ile	Thr 315	Gln	Ile	Ser	Ser	Туr 320
Val	Ala	Tyr	Ser	Asn 325	Ser	Gly	Leu	Asn	Pro 330	Leu	Val	Tyr	Val	Ile 335	Val
Gly	Lys	Arg	Phe 340	Arg	Lys	Lys	Ser	Arg 345	Glu	Val	Tyr	Arg	Val 350	Leu	Cys
Gln	Lys	Gly 355	Gly	Cys	Met	Gly	Glu 360	Pro	Val	Gln	Met	G1u 365	Asn	Ser	Met
Gly	Thr 370	Leu	Arg	Thr	Ser	Ile 375	Ser	Val	Glu	Arg	Gln 380	Ile	His	Lys	Leu
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Val	Ser	Gln	Ser 20	Ser	Gly	Cys	Pro	Asn 25	Thr	Glu	Trp	Ser	Gly 30	Trp	Leu
Asn	Val	Ile	Gln	Ala	Pro	Phe	Leu	Trp	Val	Leu	Phe	Val	Leu	Ala	Thr

Leu Glu Asn Leu Phe Val Leu Ser Val Phe Cys Leu His Lys Ser Ser

Cys Thr Val Ala Glu Val Tyr Leu Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe Trp Ala Val Thr Ile Ala Asn His 90 Phe Asp Trp Leu Phe Gly Glu Ala Leu Cys Arg Val Val Asn Thr Met 105 Ile Tyr Met Asn Leu Tyr Ser Ser Ile Cys Phe Leu Met Leu Val Ser 120 Ile Asp Arg Tyr Leu Ala Leu Val Lys Thr Met Ser Ile Gly Arg Met 135 Arg Arg Val Arg Trp Ala Lys Leu Tyr Ser Leu Val Ile Trp Gly Cys 150 155 Thr Leu Leu Ser Ser Pro Met Leu Val Phe Arg Thr Met Lys Asp 170 Tyr Arg Asp Glu Gly Tyr Asn Val Thr Ala Cys Ile Ile Asp Tyr Pro 185 Ser Arg Ser Trp Glu Val Phe Thr Asn Val Leu Leu Asn Leu Val Gly 200 Phe Leu Leu Pro Leu Ser Val Ile Thr Phe Cys Thr Val Gln Ile Leu 215 220 Gln Val Leu Arg Asn Asn Glu Met Gln Lys Phe Lys Glu Ile Gln Thr 235 Glu Arg Arg Ala Thr Val Leu Val Leu Ala Val Leu Leu Phe Val 250 Val Cys Trp Leu Pro Phe Gln Val Ser Thr Phe Leu Asp Thr Leu Leu Lys Leu Gly Val Leu Ser Ser Cys Trp Asp Glu His Val Ile Asp Val Ile Thr Gln Val Gly Ser Phe Met Gly Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly Lys Arg Phe Arg Lys Lys Ser Arg 315 Glu Val Tyr Arg Ala Ala Cys Pro Lys Ala Gly Cys Val Leu Glu Pro Val Gln Ala Glu Ser Ser Met Gly Thr Leu Arg Thr Ser Ile Ser Val 345 Glu Arg Gln Ile His Lys Leu Pro Glu Trp Thr Arg Ser Ser Gln 360

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Ile Gln Ala Pro Phe Leu Trp Val Leu Phe Val Leu Ala Val Leu Glu 35 40 45

Asn Ile Phe Val Leu Ser Val Phe Phe Leu His Lys Ser Ser Cys Thr 50 55 60

Val Ala Glu Ile Tyr Leu Gly Asn Leu Ala Val Ala Asp Leu Ile Leu 65 70 75 80

Ala Phe Gly Leu Pro Phe Trp Ala Ile Thr Ile Ala Asn Asn Phe Asp 85 90 95

Trp Leu Phe Gly Glu Val Leu Cys Arg Met Val Asn Thr Met Ile Gln 100 105 110

Met Asn Met Tyr Ser Ser Ile Cys Phe Leu Met Leu Val Ser Ile Asp 115 120 125

Arg Tyr Leu Ala Leu Val Lys Thr Met Ser Met Gly Arg Met Arg Gly 130 135 140

Val Arg Trp Ala Lys Leu Tyr Ser Leu Val Ile Trp Gly Cys Ala Leu 145 150 155 160

Leu Leu Ser Ser Pro Met Leu Val Phe Arg Thr Met Lys Asp Tyr Arg 165 170 175

Asp Glu Gly His Asn Val Thr Ala Cys Leu Ile Ile Tyr Pro Ser Leu 180 185 190

Thr Trp Gln Val Phe Thr Asn Val Leu Leu Asn Leu Val Gly Phe Leu 195 200 205

Leu Pro Leu Ser Ile Ile Thr Phe Cys Thr Val Gln Ile Met Gln Val 210 215 220

Leu Arg Asn Asn Glu Met Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg 225 230 235 240

Arg Ala Thr Val Leu Val Leu Ala Val Leu Leu Leu Phe Val Val Cys 245 250 255

Trp Leu Pro Phe Gln Ile Gly Thr Phe Leu Asp Thr Leu Arg Leu Leu 260 265 270

Gly Phe Leu Pro Gly Cys Trp Glu His Val Ile Asp Leu Ile Thr Gln 275 280 285

Ile Ser Ser Tyr Leu Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val 290 295 300

Tyr Val Ile Val Gly Lys Arg Phe Arg Lys Lys Ser Arg Glu Val Tyr 305 310 315 320

His Gly Leu Cys Arg Ser Gly Gly Cys Val Ser Glu Pro Ala Gln Ser 325 330 335

Glu Asn Ser Met Gly Thr Leu Arg Thr Ser Ile Ser Val Asp Arg Gln 340 345 350

Ile His Lys Leu Gln Asp Trp Ala Arg Ser Ser Ser Glu Gly Thr Pro
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Pro Gly Leu Leu 370

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<211> 396

<212> PRT

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<400> 841

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Val Phe Trp Gly Pro Gly Cys His Leu Ser Thr Cys Ile Glu Met Phe 20 25 30

Asn Ile Thr Thr Gln Ala Leu Gly Ser Ala His Asn Gly Thr Phe Ser 35 40 45

Glu Val Asn Cys Pro Asp Thr Glu Trp Trp Ser Trp Leu Asn Ala Ile 50 55 60

Gln Ala Pro Phe Leu Trp Val Leu Phe Leu Leu Ala Ala Leu Glu Asn 65 70 75 80

Ile Phe Val Leu Ser Val Phe Cys Leu His Lys Thr Asn Cys Thr Val 85 90 95

Ala Glu Ile Tyr Leu Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala 100 105 110

Cys Gly Leu Pro Phe Trp Ala Ile Thr Ile Ala Asn Asn Phe Asp Trp 115 120 125

Leu Phe Gly Glu Val Leu Cys Arg Val Val Asn Thr Met Ile Tyr Met 130 135 140

Asn Leu Tyr Ser Ser Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg

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Arg	Trp	Ala	a Lys 180	Leu )	ı Tyr	Ser	Leu	Val 185		e Trp	Ser	. Cys	Thr 190	Leu	Leu
Leu	Ser	Ser 195	r Pro	) Met	Leu	ı Val	Phe 200	arg	Thr	Met	: Lys	Asp 205		Arg	Glu
Glu	Gly 210	His	a Asn	ı Val	Thr	Ala 215	Cys	Val	Ile	· Val	Tyr 220	Pro	Ser	Arg	Ser
Trp 225	Glu	Val	Phe	Thr	Asn 230	Met	Leu	Leu	Asn	Leu 235	. Val	Gly	Phe	Leu	Leu 240
Pro	Leu	Ser	Ile	11e 245	Thr	Phe	Cys	Thr	Val 250	Arg	Ile	Met	Gln	Val 255	Leu
Arg	Asn	Asn	Glu 260	Met	Lys	Lys	Phe	Lys 265	Glu	Val	Gln	Thr	Glu 270	Lys	Lys
Ala	Thr	Val 275	Leu	Val	Leu	Ala	Val 280	Leu	Gly	Leu	Phe	Val 285	Leu	Cys	Trp
Phe	Pro 290	Phe	Gln	Ile	Ser	Thr 295	Phe	Leu	Asp	Thr	Leu 300	Leu	Arg	Leu	Gly
Val 305	Leu	Ser	Gly	Cys	Trp 310	Asn	Glu	Arg	Ala	Val 315	Asp	Ile	Val	Thr	Gln 320
Ile	Ser	Ser	Tyr	Val 325	Ala	Tyr	Ser	Asn	Ser 330	Cys	Leu	Asn	Pro	Leu 335	Val
Tyr	Val	Ile	Val 340	Gly	Lys	Arg	Phe	Arg 345	Lys	Lys	Ser	Arg	Glu 350	Val	Tyr
Gln	Ala	Ile 355	Cys	Arg	Lys	Gly	Gly 360	Cys	Met	Gly	Glu	Ser 365	Val	Gln	Met
Glu	Asn 370	Ser	Met	Gly	Thr	Leu 375	Arg	Thr	Ser	Ile	Ser 380	Val	Asp	Arg	Gln
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gaaaaatgag	atggcaagag	caaatcatta	tgaggactat	ggggattatt	ggagaggaga	720
ctatgaagta	aatggggtag	atggctatga	ctacagccgc	ggccagttga	ttgaagatgt	780
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gcttggtgat	atgtggggta	gattttggac	aaatctgtac	tctttgacag	ttccctttgg	960
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<400> 843

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Ala Gln Ser Thr Ile Glu Glu Gln Ala Lys Thr Phe Leu Asp Lys Phe 20 25 30

Asn His Glu Ala Glu Asp Leu Phe Tyr Gln Ser Ser Leu Ala Ser Trp 35 40 45

Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn 50 55 60

Ala Gly Asp Lys Trp Ser Ala Phe Leu Lys Glu Gln Ser Thr Leu Ala 65 70 75 80

Gln Met Tyr Pro Leu Gln Glu Ile Gln Asn Leu Thr Val Lys Leu Gln 85 90 95

Leu Gln Ala Leu Gln Gln Asn Gly Ser Ser Val Leu Ser Glu Asp Lys
100 105 110

Ser Lys Arg Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser 115 120 125

Thr Gly Lys Val Cys Asn Pro Asp Asn Pro Gln Glu Cys Leu Leu 130 135 140

Glu Pro Gly Leu Asn Glu Ile Met Ala Asn Ser Leu Asp Tyr Asn Glu 145 150 155 160

Arg Leu Trp Ala Trp Glu Ser Trp Arg Ser Glu Val Gly Lys Gln Leu 165 170 175

Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg 180 185 190

Ala Asn His Tyr Glu Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu
195 200 205

Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser Arg Gly Gln Leu Ile Glu 210 215 220

Asp Val Glu His Thr Phe Glu Glu Ile Lys Pro Leu Tyr Glu His Leu 225 230 235 240

His Ala Tyr Val Arg Ala Lys Leu Met Asn Ala Tyr Pro Ser Tyr Ile 245 250 255

Ser Pro Ile Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly Arg Phe Trp Thr Asn Leu Tyr Ser Leu Thr Val Pro Phe Gly Gln Lys 280 Pro Asn Ile Asp Val Thr Asp Ala Met Val Asp Gln Ala Trp Asp Ala 300 Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu 310 315 Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro 330 Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly 345 Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp 360 Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe 395 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys 410 His Leu Lys Ser Ile Gly Leu Leu Ser Pro Asp Phe Gln Glu Asp Asn 425 Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly 440 Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe 460 Lys Gly Glu Ile Pro Lys Asp Gln Trp Met Lys Lys Trp Trp Glu Met Lys Arg Glu Ile Val Gly Val Val Glu Pro Val Pro His Asp Glu Thr 490 Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln Phe Gln Phe Gln Glu Ala Leu Cys Gln Ala Ala Lys His Glu Gly Pro Leu His Lys Cys Asp Ile Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Phe Asn Met Leu Arg Leu

555

Gly Lys Ser Glu Pro 565 Trp Thr Leu Ala Leu Glu Asn Val Val Gly Ala 575

Lys Asn Met Asn Val Arg Pro Leu Leu Asn Tyr Phe Glu Pro Leu Phe 580

Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser Phe Val Gly Trp Ser Thr

Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser Phe Val Gly Trp Ser Thr 595 600 605

Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu 610 615 620

Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu Trp Asn Asp Asn Glu Met 625 630 635 640

Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Gln Tyr Phe Leu 645 650 655

Lys Val Lys Asn Gln Met Ile Leu Phe Gly Glu Glu Asp Val Arg Val 660 665 670

Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn Phe Phe Val Thr Ala Pro 675 680 685

Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile 690 695 700

Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn 705 710 715 720

Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr Leu Gly Pro Pro Asn Gln 725 730 735

Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val 740 745 750

Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg 755 760 765

Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu Asn Pro Tyr Ala Ser Ile 770 780

Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly Phe Gln Asn Thr Asp Asp 785 790 795 800

Val Gln Thr Ser Phe 805

<210> 844

<211> 3733

<212> DNA

<213> homo sapiens

<220>

<221> misc\_feature

<222> (40)..(40)

<223> wherein N is either a "C" or a "T". <220> <221> misc\_feature <222> (47)..(47)<223> wherein N is either an "A" or a "C". <220> <221> misc\_feature <222> (933)..(933) <223> wherein N is either a "T" or a "C". <220> <221> misc\_feature <222> (1061)..(1061) <223> wherein N is either a "G" or an "A". <400> 844 atgttctctc cctggaagat atcaatgttt ctgtctgttn gtgaggnctc cgtgcccacc 60 acggeetett teagegeega catgeteaat gteacettge aagggeecae tettaacggg 120 acctttgccc agagcaaatg cccccaagtg gagtggctgg gctggctcaa caccatccag 180 ccccccttcc tctgggtgct gttcgtgctg gccaccctag agaacatctt tgtcctcagc 240 gtcttctgcc tgcacaagag cagctgcacg gtggcagaga tctacctggg gaacctggcc 300 gcagcagacc tgatcctggc ctgcgggctg cccttctggg ccatcaccat ctccaacaac 360 ttcgactggc tctttgggga gacgctctgc cgcgtggtga atgccattat ctccatgaac 420 ctgtacagca gcatctgttt cctgatgctg gtgagcatcg accgctacct ggccctggtg 480 aaaaccatgt ccatgggccg gatgcgcggc gtgcgctggg ccaagctcta cagcttggtg 540 atctgggggt gtacgctgct cctgagctca cccatgctgg tgttccggac catgaaggag 600 tacagcgatg agggccacaa cgtcaccgct tgtgtcatca gctacccatc cctcatctgg 660 gaagtgttca ccaacatgct cctgaatgtc gtgggcttcc tgctgcccct gagtgtcatc 720 accttctgca cgatgcagat catgcaggtg ctgcggaaca acgagatgca gaagttcaag 780 gagatccaga cggagaggag ggccacggtg ctagtcctgg ttgtgctgct gctattcatc 840 atctgctggc tgcccttcca gatcagcacc ttcctggata cgctgcatcg cctcggcatc 900 ctctccagct gccaggacga gcgcatcatc gangtaatca cacagatcgc ctccttcatg 960 gcctacagca acagctgcct caacccactg gtgtacgtga tcgtgggcaa gcgcttccga 1020 aagaagtett gggaggtgta eeagggagtg tgeeagaaag ngggetgeag gteagaacee

1080

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<220> <221>

<222>

VARIANT

(354)..(354)

<223> wherein Xaa is either "Gly" or a "Glu".

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aaaaaaaaa aaa
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<211>
       391
<212>
      PRT
<213> homo sapiens
<220>
<221>
      VARIANT
<222>
      (14)..(14)
<223> wherein Xaa is either "Arg" or a "Cys".
<220>
<221>
      VARIANT
<222>
       (16)..(16)
<223> wherein Xaa is either "Asp" or a "Ala".
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<400> 845

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Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met 310 315 Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly 325 330 Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln 345 Lys Xaa Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly 355 360 Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln 375 Asp Trp Ala Gly Ser Arg Gln 385 <210> 846 <211> 3428 <212> DNA <213> homo sapiens <400> 846 caccctatcc tacactacta ggaacttgca cagtccgcct cgggcagccc aaagctcctc 60 tgcccaccct ggctcccaaa accctccaaa acaaaagacc agaaaagcac tctccaccca 120 gcagccaaac gcctccttct tgacgccagc ccccaccctc tgtctgctcg agcccaggaa 180 aggeetgaag gaacaggeeg gggaaggage cetecetete teeettgtee etceatecae 240 ccagcgccgg catctggaga ccctatggcc cgggctcact ggggctgctg cccctggctg 300 gtcctcctct gtgcttgtgc ctggggccac acaaagccac tggaccttgg agggcaggat 360 gtgagaaatt gttccaccaa cccccttac cttccagtta ctgtggtcaa taccacaatg 420 tcactcacag ccctccgcca gcagatgcag acccagaatc tctcagccta catcatccca 480 ggcacagatg ctcacatgaa cgagtacatc ggccaacatg acgagaggcg tgcgtggatt 540 acaggettta cagggtetge aggaactgea gtggtgaeta tgaagaaage agetgtetgg 600 accgacagtc gctactggac tcaggctgag cggcaaatgg actgtaattg ggagctccat 660 aaggaagttg gcaccactcc tattgtcacc tggctcctca ccgagattcc tgctggaggg 720 cgtgtgggtt ttgacccctt cctcttgtcc attgacacct gggagagtta tgatctggcc 780 ctccaaggct ctaacagaca gctggtgtcc atcacaacca atcttgtgga cctggtatgg 840

900

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<211> 673 <212> PRT

<213> homo sapiens

<400> 847

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Val Arg Asn Cys Ser Thr Asn Pro Pro Tyr Leu Pro Val Thr Val Val 35 40 45

Asn Thr Thr Met Ser Leu Thr Ala Leu Arg Gln Gln Met Gln Thr Gln 50 55 60

Asn Leu Ser Ala Tyr Ile Ile Pro Gly Thr Asp Ala His Met Asn Glu 65 70 75 80

Tyr Ile Gly Gln His Asp Glu Arg Arg Ala Trp Ile Thr Gly Phe Thr 85 90 95

Thr Asp Ser Arg Tyr Trp Thr Gln Ala Glu Arg Gln Met Asp Cys Asn 120 Trp Glu Leu His Lys Glu Val Gly Thr Thr Pro Ile Val Thr Trp Leu Leu Thr Glu Ile Pro Ala Gly Gly Arg Val Gly Phe Asp Pro Phe Leu 155 Leu Ser Ile Asp Thr Trp Glu Ser Tyr Asp Leu Ala Leu Gln Gly Ser 170 Asn Arg Gln Leu Val Ser Ile Thr Thr Asn Leu Val Asp Leu Val Trp 185 Gly Ser Glu Arg Pro Pro Val Pro Asn Gln Pro Ile Tyr Ala Leu Gln 200 Glu Ala Phe Thr Gly Ser Thr Trp Gln Glu Lys Val Ser Gly Val Arg 215 220 Ser Gln Met Gln Lys His Gln Lys Val Pro Thr Ala Val Leu Leu Ser 230 235 Ala Leu Glu Glu Thr Ala Trp Leu Phe Asn Leu Arg Ala Ser Asp Ile 245 250 Pro Tyr Asn Pro Phe Phe Tyr Ser Tyr Thr Leu Leu Thr Asp Ser Ser Ile Arg Leu Phe Ala Asn Lys Ser Arg Phe Ser Ser Glu Thr Leu Ser 280 Tyr Leu Asn Ser Ser Cys Thr Gly Pro Met Cys Val Gln Ile Glu Asp 290 Tyr Ser Gln Val Arg Asp Ser Ile Gln Ala Tyr Ser Leu Gly Asp Val 310 315 Arg Ile Trp Ile Gly Thr Ser Tyr Thr Met Tyr Gly Ile Tyr Glu Met 325 330 Ile Pro Arg Glu Lys Leu Val Thr Asp Thr Tyr Ser Pro Val Met Met 345 Thr Lys Ala Val Lys Asn Ser Lys Glu Gln Ala Leu Leu Lys Ala Ser 355 His Val Arg Asp Ala Val Ala Val Ile Arg Tyr Leu Val Trp Leu Glu Lys Asn Val Pro Lys Gly Thr Val Asp Glu Phe Ser Gly Ala Glu Ile 385 Val Asp Lys Phe Arg Gly Glu Glu Gln Phe Ser Ser Gly Pro Ser Phe 410

Glu Thr Ile Ser Ala Ser Gly Leu Asn Ala Ala Leu Ala His Tyr Ser 420 425 430

Pro Thr Lys Glu Leu Asn Arg Lys Leu Ser Ser Asp Glu Met Tyr Leu 435 440 445

Leu Asp Ser Gly Gly Gln Tyr Trp Asp Gly Thr Thr Asp Ile Thr Arg 450 455 460

Thr Val His Trp Gly Thr Pro Ser Ala Phe Gln Lys Glu Ala Tyr Thr 465 470 475 480

Arg Val Leu Ile Gly Asn Ile Asp Leu Ser Arg Leu Ile Phe Pro Ala 485 490 495

Ala Thr Ser Gly Arg Met Val Glu Ala Phe Ala Arg Arg Ala Leu Trp 500 505 510

Asp Ala Gly Leu Asn Tyr Gly His Gly Thr Gly His Gly Ile Gly Asn 515 520 525

Phe Leu Cys Val His Glu Trp Pro Val Gly Phe Gln Ser Asn Asn Ile 530 540

Ala Met Ala Lys Gly Met Phe Thr Ser Ile Glu Pro Gly Tyr Tyr Lys 545 550 555 560

Asp Gly Glu Phe Gly Ile Arg Leu Glu Asp Val Ala Leu Val Val Glu 565 570 575

Ala Lys Thr Lys Tyr Pro Gly Glu Leu Pro Asp Leu Val Val Ser Phe 580 585 590

Val Pro Tyr Asp Arg Asn Leu Ile Asp Val Ser Leu Leu Ser Pro Glu 595 600 605

His Leu Gln Tyr Leu Asn Arg Tyr Tyr Gln Thr Ile Arg Glu Lys Val 610 620

Gly Pro Glu Leu Gln Arg Arg Gln Leu Leu Glu Glu Phe Glu Trp Leu 625 630 635 640

Gln Gln His Thr Glu Pro Leu Ala Ala Arg Ala Pro Asp Thr Ala Ser
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Val

<210> 848

<211> 1082

<212> DNA

<213> homo sapiens

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<211> 353

<212> PRT

<213> homo sapiens

<400> 849

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Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala 20 25 30

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Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu

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Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu 85 90 95

Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe
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Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val 145 150 155 160

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<sup>&</sup>lt;211> 427

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> homo sapiens

<sup>&</sup>lt;400> 853

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1260

1284

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1.5	cccgac	adeca agaateteet ttaattt	27
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	<211>	18	
is È	<212>	DNA	
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The Thirt Thirt Thirth			
er : i	<400>	1232	
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	/213/	nomo sapiens	
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	3 33		18
	010		
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	222990	good occaggaact ttg	23
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₽+£				
C)	<400>	1237		
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that the the true that the				
11.59				
45, 8	<210>			
itis pi is pre	<211>			
ij <sub>2</sub> ; į	<212>			
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ij				
- <u>k</u>	<400>	1238		
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li : ii				
The state of the s		1239		
Noof N		27		
ļas ģ	<212>			
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ij	<212>		
The state that the st	<213>	Homo sapiens	
11.0	<400>	1243	
.[]		tgca aaccttagca tgcac	25
			23
, E	<210>		
	<211>		
:= <u> </u> ;	<212>		
	<213>	Homo sapiens	
Total Teach Teach Towns Mr.	<220>		
i de la companya de l	<221>	misc_feature	
		(12)(12)	
:= =	<223>	wherein "n" equals a C3 phosphoramidite linker.	
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                                                                            27
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           wherein "n" equals a C3 phosphoramidite linker.
ų.
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<221>
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    <222>
#
           (21)..(21)
   <223>
          wherein "n" equals a C3 phosphoramidite linker.
Fiz E
T,
| m2 5
    <400> 1247
cccggsctct tccttcangc ntttcct
                                                                           27
41.1
---
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          1248
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          DNA
    <213>
          Homo sapiens
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          (12)..(12)
          wherein "n" equals a C3 phosphoramidite linker.
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   <400> 1248
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                                                                           27
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          1249
   <211>
          25
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          DNA
   <213> Homo sapiens
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    tacctaaata aataataaaa gccag
                                                                         25
    <210> 1250
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    <400> 1250
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                                                                         27
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          27
<212>
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          Homo sapiens
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<222>
          (19)..(19)
Į
    <223> wherein "n" equals a C3 phosphoramidite linker.
Œ
   <400> 1251
===
   agacttcacc tcttggcanc ttggctt
H
                                                                        27
L.
    <210> 1252
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    <212> DNA
    <213> Homo sapiens
    <400> 1252
    ctgcatgttg ctgaagggtg aaaga
                                                                        25
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          Homo sapiens
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          (16)..(16)
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                                                                            27
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           (9)..(9)
    <223> wherein "n" equals a C3 phosphoramidite linker.
    <220>
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           (19)..(19)
THE REAL PROPERTY.
    <223> wherein "n" equals a C3 phosphoramidite linker.
    <400> 1254
    ttaccctang gctgacctnc caggaac
                                                                            27
(H
    <210> 1255
    <211> 25
    <212> DNA
hark.
    <213> Homo sapiens
<400> 1255
    tcacctggct cctcaccgag attcc
                                                                            25
ļ.,
i i
    <210> 1256
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          (19)..(19)
    <223> wherein "n" equals a C3 phosphoramidite linker.
    <400> 1256
    tatttcagnc cactgacang gcctcag
                                                                           27
```

¥

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           Homo sapiens
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    accttcatag agggtataat aaaag
                                                                            25
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           DNA
    <213>
          Homo sapiens
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    aagagtttgt ttgaggaaag ggttt
                                                                           25
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          1259
    <211>
          27
LI LI
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          DNA
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           Homo sapiens
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    <223>
           wherein "n" equals a C3 phosphoramidite linker.
E.
m= i=
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                                                                           27
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    <212>
          DNA
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    <223>
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          1261
    <211>
          25
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	<212>		
	<213>	Homo sapiens	
	<400>	1262	
	atccto	gaatt atccaagtgg gccct	25
	010		
	<210>		
	<211> <212>		
		Homo sapiens	
m k			
:: #  -  -	<400>		
:: F	cagcag	gaaa caaataacaa gtatc	25
ment than and that that the pr	<210>	1264	
14	<211>		
T HOUSE	<212>		
- Harr	<213>		
= i:	<220>		
Ē	<221>	misc_feature	
- d	<222>	(18)(18)	
There well from	<223>	wherein "n" equals a C3 phosphoramidite linker.	
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	-210	1065	
	<210> <211>	1265 27	
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		Homo sapiens	
	-220-		
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		wherein "n" equals a C3 phosphoramidite linker.	
		The proops of an area of the proops of the proof of the proops of the proof of the proops of the proof	
	<400>	1265	
	ctggga	cctg ctgnacagag tgctgcc	27
		1266	
	<211>	27	

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          25
ļu: L
   <212>
          DNA
<213>
          Homo sapiens
<400> 1267
                                                                           25
   gagccctcct ctgccgtgtc atcaa
ų,
17.
Į, į
   <210> 1268
    <211>
          25
Œ
   <212>
          DNA
ļ.
   <213> Homo sapiens
1.1
   <400> 1268
                                                                           25
    agatctgaac atcaccgcct gcatc
la k
-
    <210>
          1269
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          Homo sapiens
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          (17)..(17)
          wherein "n" equals a C3 phosphoramidite linker.
    <400> 1269
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    cactgggcaa atcngcnggg ctccccc
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            Homo sapiens
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            wherein "n" equals a C3 phosphoramidite linker.
    <400> 1270
    gtnggaatga caggtngaag ggagcca
                                                                                27
j-Ł
The state of the state of
    <210>
            1271
    <211>
            27
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           DNA
<213>
           Homo sapiens
W.
1
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    <222>
           (16)..(16)
las je
    <223>
            wherein "n" equals a C3 phosphoramidite linker.
fine,
F.,
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                                                                                27
first
first
---
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           Homo sapiens
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                                                                                25
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           Homo sapiens
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                                                                                25
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    <210>
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                  <223>
                                             wherein "n" equals a C3 phosphoramidite linker.
                  <400> 1275
                  attectteae teatntatna aacaaaa
                                                                                                                                                                                                                                                                                                         27
The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
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                 <211>
                                            25
                 <212>
                                            DNA
                 <213>
                                           Homo sapiens
100 mm
                 <400> 1276
Ç.
                tacgttgagc gatgagcccc aggtt
                                                                                                                                                                                                                                                                                                        25
35
ļ.: <u>.</u>
                <210> 1277
<211> 27
                <212>
                                          DNA
Ļij
                <213>
                                           Homo sapiens
lar f
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                <222> (16)..(16)
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                                          (19)..(19)
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                                          wherein "n" equals a C3 phosphoramidite linker.
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               acaggggctg gggatngcna aatacac
                                                                                                                                                                                                                                                                                                      27
               <210> 1278
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                                       22
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              <213> Homo sapiens
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gtggtg	gggca cggagtcctc ac	22
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gtcagg	gagg ggcncacctg ggcgcgg	27
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.400	1000	
		0.7
tttttg	mage ettaaaacee tteette	27
-21As	1201	
<b>\Z13</b> /	nomo sapiens	
~100×	1291	
		25
gcagaa	igety teetytetee tyggt	25
~21N\	1292	
<b>\Z13</b> /	nomo sapiens	•
<220h		
	misc foaturo	
	· · · · · · · · · · · · · · · · · · ·	
-223/	whotein it equals a co-phosphotamidite ithker.	
<400>	1282	
	•	27
	<pre></pre>	<pre>&lt;221&gt; misc_feature &lt;222&gt; (14)(14) &lt;223&gt; wherein "n" equals a C3 phosphoramidite linker.  &lt;400&gt; 1279 gtcagggagg ggcncacctg ggcgcgg  &lt;210&gt; 1280 &lt;211&gt; 27 &lt;212&gt; DNA &lt;213&gt; Homo sapiens  &lt;220&gt; &lt;221&gt; misc_feature &lt;222&gt; (7)(7) &lt;223&gt; wherein "n" equals a C3 phosphoramidite linker.  &lt;400&gt; 1280 ttttgnagc cttaaaaccc ttccttc  &lt;210&gt; 1281 &lt;211&gt; 25 &lt;212&gt; DNA &lt;213&gt; Homo sapiens  &lt;220&gt; (221) misc_feature &lt;222&gt; (7)(7) &lt;223&gt; wherein "n" equals a C3 phosphoramidite linker.</pre> <400> 1280 ttttgnagc cttaaaaccc ttccttc <210> 1281 <211> 25 <212> DNA <213> Homo sapiens <400> 1281 gcagaagctg tcctgtttcc tgggt <210> 1282 <211> 27 <212> DNA <213> Homo sapiens Homo sapiens

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           1283
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           Homo sapiens
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           misc_feature
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           (13)..(13)
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           wherein "n" equals a C3 phosphoramidite linker.
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    cattgcacca aanctggatg gc
                                                                             22
    <210>
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    <211>
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           DNA
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<220>
    <221>
           misc_feature
    <222>
           (7)..(7)
Martin Brown
    <223>
           wherein "n" equals a C3 phosphoramidite linker.
ų.į
17
    <220>
1
    <221>
           misc_feature
    <222>
g:
           (15)..(15)
           wherein "n" equals a C3 phosphoramidite linker.
rıs k
fi,
Ľ,
    <400> 1284
    gctttcnggt ggtgncagtg cccagtc
                                                                             27
1
i ek
    <210>
          1285
    <211>
          25
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    <213>
          Homo sapiens
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    gagcgaaggg ctggctgagg tcatg
                                                                             25
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   accttttgct tgatttttca ctgta
                                                                            25
   <210> 1287
   <211> 25
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                                                                         25
    <210> 1288
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    acccacagca ccctgctnga ccgtctc
                                                                         27
ļu.
<210> 1289
    <211> 27
<212>
          DNA
<213>
         Homo sapiens
ų.į
<220>
Ç.
    <221>
          misc_feature
Ħ
    <222>
          (16)..(16)
2:4
    <223>
          wherein "n" equals a C3 phosphoramidite linker.
<400> 1289
    agggttgcag ggaganctgg gatgagg
                                                                         27
122
    <210> 1290
    <211> 27
    <212>
          DNA
    <213>
          Homo sapiens
    <220>
    <221> misc_feature
    <222>
          (11)..(11)
          wherein "n" equals a C3 phosphoramidite linker.
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   gctgggatga ngyctggggt gctgcct
                                                                         27
   <210> 1291
    <211>
          25
    <212> DNA
   <213> Homo sapiens
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		1291 tgga gaaaaactg tgctg	25
	getete	lygu guuduudeeg egees	
	<210>	1292	
		27	
	<212>	DNA	
		Homo sapiens	
	<220>		
		misc_feature .	
	<222>	(17)(17)	
	<223>	wherein "n" equals a C3 phosphoramidite linker.	
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	<400>	ctcc aagtctntgt cccacaa	27
	CCCCCC	cee aageetnege eecacaa	
	<210>	1293	
Hc.		25	
15=4 11=4	<212>	DNA	
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	<400>	1293	25
4.11	gaagag	rggaa ctgaggcagg gacag	25
fit	<210>	1294	
	<211>		
# L.L	<212>	DNA	
The gives the company of the company	<213>	Homo sapiens	
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i, i	<221>	misc_feature	
	<222>	(15)(15)	
ļs;ķ	<223>	wherein "n" equals a C3 phosphoramidite linker.	
	<220>		
		misc_feature	
		(18)(18) wherein "n" equals a C3 phosphoramidite linker.	
	<223>	wherein heddars a co phobbiotement	
	<400>	1294	
		tgcta cgtanatntg aggcatc	27
	555		
	<210>	1295	
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	<400>		2.5
	cccag	cgctg gggaaagaaa ggaca	25

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           Homo sapiens
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                                                                           25
    <210>
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    <211>
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    <212>
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    <213> Homo sapiens
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1=4
129
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<223>
          wherein "n" equals a C3 phosphoramidite linker.
M
ų,
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Ľ1
    aagctggaan cctcnaggat gggttca
                                                                           27
æ
n i
    <210>
          1298
    <211>
           22
<212>
          DNA
    <213>
           Homo sapiens
ar k
    <400> 1298
    aagctctacc acgccttctc ag
                                                                           22
    <210> 1299
    <211> 27
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    <213>
          Homo sapiens
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    <220>
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          (13)..(13)
   <223> wherein "n" equals a C3 phosphoramidite linker.
```

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    ggaacttgtn ctnctggtcc cagagca
                                                                            27
    <210> 1300
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    <213> Homo sapiens
    <400> 1300
    tactggcgaa gacagcggcg atggg
                                                                            25
    <210> 1301
    <211>
          22
    <212>
           DNA
    <213>
           Homo sapiens
    <400> 1301
    ccagcaggag agccaggacc ca
                                                                            22
ļ.
And The Bush Some
    <210> 1302
    <211>
          22
    <212>
           DNA
    <213> Homo sapiens
4.4
<400> 1302
[]
    ccaagcgcaa ggtgagcagg gg
                                                                            22
¥
ja þ
    <210>
          1303
<211>
          22
    <212>
           DNA
    <213>
           Homo sapiens
ur -
    <220>
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    <222>
           (12)..(12)
    <223>
           wherein "n" equals a C3 phosphoramidite linker.
    <400> 1303
    aggtcggacc ancttttccc aa
                                                                            22
    <210> 1304
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    <212> DNA
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          wherein "n" equals a C3 phosphoramidite linker.
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    <223>
           wherein "n" equals a C3 phosphoramidite linker.
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    tccctatctt tgcnacnctn atgctgt
                                                                             27
    <210> 1305
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          DNA
    <213>
          Homo sapiens
ļ...L
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    <221>
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    <222>
           (19)..(19)
    <223>
           wherein "n" equals a C3 phosphoramidite linker.
1.75
Į.į
Tall the
    <400> 1305
acccatactg acccttttng caagicc
                                                                             27
Ħ
ar c
    <210>
           1306
II.
    <211>
           27
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           DNA
    <213>
           Homo sapiens
je: h
    <220>
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    <222>
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           wherein "n" equals a C3 phosphoramidite linker.
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           misc_feature
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           (21)..(21)
           wherein "n" equals a C3 phosphoramidite linker.
    <223>
    <400> 1306
                                                                             27
    agagcagttn gaggtcaggt ncaggga
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           1307
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           DNA
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           wherein "n" equals a C3 phosphoramidite linker.
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                                                                           27
    <210>
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   <211>
          27
    <212>
          DNA
[]
    <213>
           Homo sapiens
    <220>
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          misc_feature
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          (10)..(10)
    <223> wherein "n" equals a C3 phosphoramidite linker.
ļ==‡
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    <221>
          misc_feature
<222>
          (14)..(14)
    <223> wherein "n" equals a C3 phosphoramidite linker.
i, j
fir.j
    <400> 1309
    gctgtgaagn tcgnggagtt gcccacc
                                                                           27
    <210> 1310
    <211>
          22
    <212> DNA
    <213> Homo sapiens
    <400> 1310
    aaggcrggga tggggactcc tg
                                                                           22
    <210>
          1311
    <211>
           22
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          Homo sapiens
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          (3)..(3)
```

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    tgnggccacc ccagctgtgt ca
                                                                         22
    <210> 1312
    <211> 25
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    <213> Homo sapiens
    <400> 1312
    atgtgtgtca cgttctgcca tcacc
                                                                         25
    <210> 1313
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    <221>
          misc_feature
    <222>
          (17)..(17)
    <223>
          wherein "n" equals a C3 phosphoramidite linker.
H
<400> 1313
D.
   atctggaact tatagtnttg aaaagaa
                                                                         27
42 ±
   <210>
         1314
<211>
          27
E.
    <212>
          DNA
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          Homo sapiens
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          (14)..(14)
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    <220>
    <221> misc_feature
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    <223> wherein "n" equals a C3 phosphoramidite linker.
   <400> 1314
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                                                                        27
   <210> 1315
    <211>
         25
   <212> DNA
   <213> Homo sapiens
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£

		1315	
	aagtag	acaa ggaatgggtg tgaaa	25
	<210>		
	<211>		
	<212>		
	<213>	Homo sapiens	
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		(11)(11)	
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	<220>		
		misc_feature	
		(13)(13)	
		wherein "n" equals a C3 phosphoramidite linker.	
		of the state of th	
⊫*k			
Ci	<220>		
£1		misc_feature	
120		(15)(15)	
U	<223>	wherein "n" equals a C3 phosphoramidite linker.	
onth teast cools than your			
i Fe	<220>		
		misc_feature	
#	<222>	(19)(19)	
ļ-4	<223>	wherein "n" equals a C3 phosphoramidite linker.	
FI.S			
The Tree of the	<400>	1316	
L.		tcac nantnaaant tagtagc	27
fir i			- '
ļa= <b>Ļ</b>			
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	<211>		
	<212>	Homo sapiens	
	\Z13>	HOMO Sapiens	
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	04.0	4040	
	<210>	1318	
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	\Z_1J/	HOMO DAPIGHS	
	<400>	1318	
		taaa tgactcagaa taatg	25
	-010:	1210	
	<210>	1319	
	\alpha \cdot 1 \cdot 2	$A \cdot I$	

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                                        (16)..(16)
                                        wherein "n" equals a C3 phosphoramidite linker.
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               <210>
                                      1320
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                                       Homo sapiens
               <220>
               <221>
                                        misc_feature
               <222>
                                         (9)..(9)
 1
                                        wherein "n" equals a C3 phosphoramidite linker.
               <223>
The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
               <220>
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                                        misc_feature
 <222>
                                         (19)..(19)
 <223>
                                         wherein "n" equals a C3 phosphoramidite linker.
 G1
Œ
12:2
               <400> 1320
27
               cttggtaana agccccatna attcttc
la f
The state of
               <210> 1321
Har &
               <211>
                                       27
               <212>
                                      DNA
               <213>
                                       Homo sapiens
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                                       misc_feature
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                                        wherein "n" equals a C3 phosphoramidite linker.
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               <222>
                                        (15)..(15)
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                                        wherein "n" equals a C3 phosphoramidite linker.
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                                                                                                                                                                                                                                                                                  27
               ggntggcacc gaggntgcag cagccac
               <210> 1322
               <211> 27
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                                                                           27
    aacctcnccg gncatgggct ggaaaca
    <210> 1323
          27
    <211>
ļ=£
    <212>
          DNA
    <213>
          Homo sapiens
W.
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Trans.
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1 5
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           (2)..(2)
U
          wherein "n" equals a C3 phosphoramidite linker.
    <223>
;;;
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þ::‡
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           (18)..(18)
    <223> wherein "n" equals a C3 phosphoramidite linker.
1
h-L
    <400> 1323
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    tntcttggac agatgttnat tatgaaa
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          DNA
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          wherein "n" equals a C3 phosphoramidite linker.
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    <211> 27
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                                                                         27
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          25
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<213>
          Homo sapiens
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ų,
Ľ
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#
    <211>
          25
   <212>
          DNA
ļ::±
   <213> Homo sapiens
1
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          1328
    <211>
          25
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          Homo sapiens
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          DNA
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          misc_feature
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          (10)..(10)
    <223> wherein "n" equals a C3 phosphoramidite linker.
```

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min and and and and and and and and and an	<400> tatgaa	1329 acgn gtaccanttc tatcccc	27
	<210><211><211><212><213>	39	
		1330 acga cggccagtag tteeteetee teeeteaet	39
		DNA Homo sapiens	
		1331 acga cggccagtgg cattcacagg tgattcagt	39
	<400>	39 DNA Homo sapiens	20
To an an an an an an an an an an an an an	<210><211><212>	39	39
	<213> <400>	Homo sapiens 1333	
		acga cggccagttt ctgggcttta ccctctctc	39
	<210><211><211><212><213>	1334 39 DNA Homo sapiens	
	<400>	1334	. 2.0
	cgtaaa	acga cggccagtcc aggtgcagga ttaacagac .	39
	<210> <211>	1335 39	

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	<213>	Homo sapiens			
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	_	5 55 5			33
	<210>	1337			
	<211>	38			
	<212>	DNA Homo sapiens			
ije k	\213/	nomo saprens			
	<400>	1337			
ilias fi		acga cggccagtca	gtgagatctt	gccactgc	38
terriff There would thereft thereft					
115					
Pig.	<210>	1338			
i i i	<211> <212>	39			
(II		Homo sapiens			
#: · *	\Z1J/	nomo saprens			
las is	<400>	1338			
	tgtaaa	acga cggccagtca	ggcagacaat	gatgtgatg	39
that they bear that their					
	<210>	1339			
	<210>	39			
ļas k	<212>	DNA			
		Homo sapiens			
		-			
	<400>	1339			
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	tgtaaa	acga cggccagtga	ggctccagac	tctcctgtt	39
jant. P=5					
Terr of the second seco	<210>	1344			
477 F		39			
	<212>				
u.i	<213>	Homo sapiens			
II. F	<400>	1344			
Ç1	tgtaaa	acga cggccagtca	ttgcctagaa	acctttgca	39
ii jare					
	<210>	1345			
E.	<211>	39			
Lif	<212>				
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-=   <sub> </sub> -	<400>	1345			
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		Homo sapiens			
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	<210>	1350			
ilas F	<211>	39			
1	<212>	DNA			
ore one who was the from the front t	<213>	Homo sapiens			
	400	1250			
	<400>	1350 acga cggccagtgg	attatataaa	agaggtgg	39
127	tytaaa	acya cyyccaytyy	geegeacace	acacccegg	
41					
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#	<211>	39			
ļa• <b>k</b>	<212>	DNA			
r.	<213>	Homo sapiens			
The first test from	<400>	1351			
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1	-9		3 33	3 3 3	
ļur ļi					
		1352			
	<211>	39			
	<212>				
	<213>	Homo sapiens			
	<400>	1352			
	tgtaaa	acga cggccagtca	cttgtggaaa	gcacacaga	39
	<210>	1353			
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	~213/	Homo Babrens			
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	<210>	1356			
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в.	<213>	Homo sapiens			
The state well there were the state of	<400>	1356			
ika# F™k		acga cggccagtca	aggtggacag	tcttcggta	39
lana ji Hiri B	3		99-999		33
lite Lite					
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